Workshop Report

Contract GRA1001
International Workshop: Enteric CH₄ mitigation using animal selection, genetics and genomics

16-17 May 2011
Auckland, New Zealand

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Input has also been provided by John McEwan (AgR), Lynette Mitchell (AgR), Helen Mathias-Davis (AgR) and Kate Parlane (NZAGRC).

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All photographs and diagrams were provided courtesy of the speakers and are taken from their presentations.

All responsibility for any remaining errors or omissions rests with the authors.

Disclaimer
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EXECUTIVE SUMMARY - GENERAL

Purpose
- Key researchers from around the world met and discussed the potential for reducing methane emissions and emissions intensity (emissions per unit product) by capitalising on animal to animal genetic variation in both cattle and sheep
- This was part of a Global Research Alliance initiative into livestock research which had previously identified as a priority “the setting up a network on animal breeding approaches to reduce methane emissions”

Goals
- common protocols for measurement of CH$_4$ emissions(and associated traits) suitable for genetic and genomic research
- calibrations of measurement differences between countries
- co-measurement of appropriate correlated and productive traits
- formalised protocols for collection and storage of DNA from all animals measured
- protocols for collection and storage of rumen samples from all animals measured
- criteria for data sharing by all contributing parties

Outcomes
- The workshop participants clearly indicated that they felt the workshop was useful and was novel in that it placed researchers from many different countries and disciplines in the same venue to address a common problem for the first time
- The participants identified a need for common defined measurement protocols, regular meetings to exchange information, and the significant potential for joint work across countries
- It was identified that proper breeding objectives are required and that potential exists for inclusion of GHG traits immediately given an agreed shadow carbon price
- A large portion of the meeting focused on CH$_4$ and feed intake measurement technology and appropriate breeding objectives and data transformations
- Evidence was presented that indicate genetic increases in reproduction efficiency and survival, and decreases in age at puberty and disease will reduce emissions intensity per unit product and significant changes are currently occurring via genetic selection
- There was general consensus that respiration chambers are the “gold standard” for measuring methane emissions but suffer from cost and limitations in animal numbers that can be processed or repeatedly measured
- There was general agreement that if rapid industry uptake was to occur then reducing emissions intensity per unit of output was the most economically effective outcome rather than total emissions per individual

Actions
- A number of action points around networking and information sharing were identified
- Addressing the outcomes identified at the Workshop, would be expedited by a white paper addressing the measurement protocol needs and summarising work that is recently completed, underway or planned
- There was clear acceptance that given the cost and difficulty of the experiments it should be routine to collect host DNA samples and also rumen samples and that formal links needed to be maintained to these research areas
- While currently liveweight/carcass weight is used as a proxy for intake which in turn is used as a proxy for methane emissions in IPCC inventory calculations, a rapid CH$_4$ measurement is required as a genomic selection tool given the number of animals required when repeated measurements are necessary
- The next meeting is planned to be April 2012 in Australia
EXECUTIVE SUMMARY - SCIENCE

Data reporting

- While a considerable amount of data was presented there is a lack of scientific clarity, due to a need for calibration between techniques and protocols coupled with the potential for GxE interactions with age, feedstuff, feeding level and environment.

There was also confusion due to the wide variety of data manipulation and transformations used, which makes experimental comparisons difficult.

This was added to by the fact that many of the measurements reported were in fact only point measurements whereas the trait of interest (breeding objective) was typically emissions or intake over a year for a breeding individual and its offspring.

Problems associated with data reporting can be addressed by:

- Reporting “raw” results as well as “transformed” results in publications
- Pooling raw data sets and undertaking meta analyses
- Repeating measurements on animals at different ages
- Systematically exploring potential GxE interactions
- Calibration between different measurement techniques

Selection potential

- Intake has a heritable component that is independent of liveweight (and liveweight change) in both cattle & sheep, which can be changed by selection. Similarly, methane emissions differ between individuals even after adjustment for intake.

The heritable component of intake that is independent of liveweight and liveweight changes (in both cattle & sheep) can be changed by selection;

- intake is expressed as RFI but the method of calculation varies and it appears that adjusting for liveweight decreases the intake variance but not the heritable fraction
- given that feed costs are a significant proportion of grazing enterprises (typically ~40%) and methane production is related to feed intake it would be expected that animals with lower “adjusted feed intake” should also produce less methane and this would be an additional benefit
- direct tests are more equivocal in their results and evidence was presented that measurement of intake (independent of liveweight) at one age and forage type may only be poorly related at other ages/seasons/forage types
- further work is required

Phenotyping

- Methane emissions differ between individuals even after adjustment for intake.

  - this was repeatable across ages and forage types (Pinares et al) albeit repeatability while high on consecutive measurement days dropped markedly in measurements separated by several weeks or months
  - this indicated that several measurements separated in time would bring significant benefits if the objective was to decrease overall methane production
  - evidence was presented that CH\textsubscript{4} emission differences (adjusted for liveweight or intake) were also heritable as well (Hegarty, Robinson et al)
  - adjusting methane emissions for intake or liveweight reduced the variance and the repeatability and heritability
  - as noted previously what was less clear were the overall relationships between the traits given the variety of measurement methods, protocols and adjustments used and this needs results to be presented on a common format and where practicable merged and meta-analyses conducted
Methodologies

- Technologies for rapid measurement of CH₄ emissions are required
  - “Butter boxes” offer potential in sheep to reduce cost and allow repeated measurement in grazing animals especially sheep but need more comprehensive calibration and may have animal welfare implications
  - C-Lock and laser based systems offer potential for repeated measurements in animals regularly being handled and fed e.g. in residual feed intake facilities or milking parlours if they can be properly calibrated

- The most appropriate methods for rumen contents collection and storage are awaiting results from a detailed sampling protocol study
  Protocols are expected to become available in the short to medium term (approximately 6-12 months)

- With relation to feed intake measurement technology and appropriate breeding objectives and data transformations;
  - while a considerable amount of data was presented (see actual presentations) there is a lack of scientific clarity, due to a need for calibration between techniques and protocols coupled with the potential for GxE interactions with age, feedstuff, feeding level and environment
  - there was also confusion due to the wide variety of data manipulation and transformations used, which makes experimental comparisons difficult
  - this was added to by the fact that many of the measurements reported were in fact only point measurements whereas the trait of interest (breeding objective) was typically emissions or intake over a year for a breeding individual and its offspring
SECTION 1  BACKGROUND

This project was proposed as a vehicle to further develop a network of researchers and organisations involved in efforts to mitigate CH₄ animal emissions, within the framework of the Global Research Alliance (GRA).

The primary goal was to establish and standardise protocols for CH₄ mitigation research, in the areas of animal selection, genetics and genomics. In addition, the workshop was undertaken to develop consistent data and sample storage protocols in order to underpin the research.

The broad goals of the workshop were to:
- identify common protocols for measurement of CH₄ emissions suitable for genetic and genomic research and where necessary arrange for suitable calibrations of measurement differences between countries
- ensure that appropriate correlated and productive traits are also co-measured on individuals
- evaluate and formalise protocols for collection and storage of DNA from all animals measured
- discuss protocols for collection and storage of an appropriate rumen sample from all animals measured
- define criteria by which data can be shared by all contributing parties

While the primary focus of the workshop was enteric CH₄ emissions, a secondary focus was residual feed intake (RFI) as this is moderately heritable and will respond to selection, which will potentially result in reduced emissions intensity per unit product.

Both CH₄ emissions and RFI are currently inherently difficult to measure, and require relatively sophisticated equipment along with very well-designed, robust experimental methods to undertake.

A likely industry application of this research is via genomic selection. For this to be successful thousands of animals per species must be genotyped and/or sequenced in the research phase.

This will only be possible if all international parties pool all their available information and research into cheaper measurement methods and suitable proxy measurements is undertaken. The default position is that this information will be placed in the public domain free of any IP entanglements.

Workshop participants

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<tr>
<th>Name</th>
<th>Institution</th>
<th>Role</th>
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<tr>
<td>Peter Amer</td>
<td>AbacusBio, New Zealand</td>
<td>Speaker</td>
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<td>Mark Aspin</td>
<td>PGgRC, New Zealand</td>
<td>Chair</td>
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<td>Graeme Attwood</td>
<td>AgResearch, New Zealand</td>
<td>Chair</td>
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<td>Alexandre Caetano</td>
<td>EMBRAPA, Brazil</td>
<td>Speaker</td>
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<td>Kristi Cammack</td>
<td>University of Wyoming, USA</td>
<td>Speaker</td>
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<td>Harry Clark</td>
<td>NZAGRC, New Zealand</td>
<td>Speaker</td>
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<td>Steve Davis</td>
<td>ViaLactia, New Zealand</td>
<td>Observer</td>
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<td>Tom Davison</td>
<td>Meat &amp; Livestock, Australia</td>
<td>Observer</td>
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<td>Dominique Francois</td>
<td>INRA, France</td>
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<td>John Goopy</td>
<td>Department of Primary Industries, Australia</td>
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<td>Roger Hegarty</td>
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<td>Dorothea Heimeier</td>
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<td>Observer</td>
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<td>Julian Hill</td>
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<td>Observer</td>
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<td>Sandra Kittelmann</td>
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<td>Hutton Oddy</td>
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<td>Cesar Pinares</td>
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<td>Roel Veerkamp</td>
<td>Wageningen University, The Netherlands</td>
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<td>Philip Vercoe</td>
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<td>Garry Waghorn</td>
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<td>Guangyong Zhao</td>
<td>China Agricultural University (CAU), China</td>
<td>Observer</td>
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SECTION 2    SPEAKERS

The workshop assembled national and international scientists involved in methane and RFI research. This included scientists involved in measuring CH\textsubscript{4} emissions, RFI, the genetic and genomic components of both methane emissions and RFI. The Workshop was also attended by scientists involved in researching rumen biology and its association with CH\textsubscript{4} emissions. In addition, experts in quantitative genetics and animal production systems were included.

Peter Amer: Senior consultant with Abacusbio Limited, New Zealand, a company developing new business opportunities, and providing consultancy services to agribusinesses. Peter specialises in strategy, design and implementation of genetic improvement technologies for farmed terrestrial and aquaculture livestock. He has specific expertise in the formulation of breeding objectives, development of mating plans for commercial breeding programmes, development of genetic evaluation systems and the incorporation of genomic information into genetic evaluation results.

Donagh Berry: Principal Quantitative Geneticist at Teagasc, Moorepark in Ireland. Donagh’s research focuses on primarily genetics and genomics in dairy and beef cattle as well as sheep with a particular interest in national breeding objectives and genetic/genomic evaluations. His specialist areas include Feed efficiency in cattle and the interactions between genotype and environment. Given the considerable discussions on feed efficiency and environmental footprint Donagh’s interest in breeding for these traits in a balanced approach has intensified.

Alexandre Caetano: Scientist, EMBRAPA, Brazil. Alexandre was heavily involved in the bovine sequencing project, which identified 35,000 SNPs used for Genome wide association studies of productive traits in cattle. His work has discovered and validated SNPs that cause disease, and others which give resistance in Nelore and Gir cattle.

Kristi Cammack: Assistant Professor, University of Wyoming, USA. Kristi’s Primary research focus is establishing a nationally recognized Animal Breeding and Genetics program around integrating quantitative and molecular genetics techniques. She is specifically interested in RFI.

Harry Clark: Director NZAGRC, Palmerston North, New Zealand. Since 2001 Harry has been the leader of a research team quantifying enteric methane emissions from New Zealand ruminants and researching practical methods for reducing methane emissions from grazing ruminants. He is responsible for compiling the New Zealand agricultural methane emissions inventory and is a member of MAF’s technical advisory group for the proposed Emissions Trading Scheme and a member of MAF’s Research and Innovation technical working group.

Dominique Francois: Co-leader of a Small Ruminant Genetics team, INRA, Toulouse, France. Dominique’s primary research interest is quantitative genetics and the introduction of genomics tools in selection programmes. His specific research interest is feed efficiency in meat sheep and its relationship with other traits. Dominique also has a strong interest in the genetics of adaptation in sheep.

Roger Hegarty: Until recently, Principal Research Scientist in Industry and Investment NSW, Australia and currently, Professor of Animal Nutrition at the University of New England. Roger initiated Australia’s first workshop that engaged science, government and the ruminant industries, in order to begin to understand animal greenhouse gas emissions. Since then he has developed Australia’s leading team of animal scientists addressing management of enteric methane.
Sandra Kittelmann: Scientist, AgResearch Grasslands, New Zealand. Sandra’s background lies in molecular microbial ecology and microbiology. Sandra’s PhD at the Max Planck Institute for terrestrial microbiology, Marburg, Germany, focussed on the degradation of chlorinated carbon compounds by dehalorespiring bacteria. Since arriving at AgResearch in 2008 she has been studying the diversity and structure of ciliate protozoal and anaerobic fungal communities in the rumen environment. Sandra’s recent research is directed towards the identification of prokaryotic and eukaryotic microbial populations beneficial to methane mitigation.

John McEwan: Principal Scientist, AgResearch Invermay, New Zealand. John has a very strong background in genetic selection of sheep. He was also closely involved in the international bovine genome sequencing project. John’s current research includes sequencing the ovine genome, creation of a 60K SNP chip, and implementing genome wide selection in sheep. His expertise is specifically around sheep productive traits, including enteric CH4.

Stephen Moore: Professor, University of Alberta, Edmonton, Canada. Steve’s research program is aimed at identifying genes and gene pathways contributing towards quantitative traits in cattle. His research over the past decade has identified bovine chromosomal regions with loci affecting traits such as growth and morphology, yield, fat content and tenderness. Both structural (linkage and physical mapping) and functional genomics approaches are being developed to refine these results and identify the actual genes behind the quantitative traits. Steve’s research interests include RFI.

Cesar Pinares: Senior Research Scientist at AgResearch Grasslands, Palmerston North (NZ). Cesar is the project leader of the PGGRC program of exploiting animal-to-animal variation for methane emission mitigation. He is currently responsible for the management and application of respiration chambers and the SF6 tracer techniques for methane emission measurements from sheep and cattle. Cesar was the first to report on heritability and repeatability of the methane emission trait in sheep and has interest in the development of non-invasive methods of selecting grazing ruminants for higher feed efficiency and lowered GHG emission intensity.

Dorothy Robinson: Senior Research Scientist at NSW Industry and Investment and the National Centre for Rural Greenhouse Gas Research, University of New England, Australia. Dorothy’s research career includes developing one of the first general-purpose programs using REML methodology to estimate variance components and predict fixed and random effects. She has also been involved in the design of complex integrated research projects to estimate numerous treatment and genetic effects for a number of traits, including RFI. As part of the Armidale methane team, Dorothy’s recent work has included the analyses of methane emissions from respiration chambers and portable chamber measurements of grazing animals, including relationships with feed intake and liveweight, volatile fatty acids, and the assessment of repeatability and heritability.

Andrew Thompson: Senior Research Scientist in Sheep Production Systems at the Department of Agriculture in Western Australia. Andrew is Associate Professor of Animal Science at Murdoch University and leader of the Sheep CRC program ‘Transforming sheep and their management’. His expertise is mostly related sheep grazing systems and applied reproduction in sheep but current interests in improving overall maternal efficiency through genetics and management and its links with both adaptation/fitness and methane emissions intensity. Andrew is also involved in projects to establish genetic parameters for feed use efficiency and methane emissions and demonstrating the potential for both genetics and pasture selection to reduce methane emissions.
**Roel Veerkamp:** Group leader, Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, The Netherlands. Roel previously worked at the Scottish Agricultural College (SAC) in Edinburgh, UK, developing selection tools for UK breeding programs. Since moving to Wageningen UR, his research has focused on numerical methods to improve the application of animal breeding (including genomics information), negative effects of selection for dairy type, and genetics of the feed utilisation complex. Roel is the Coordinator of the EU project “RobustMilk”, where 5 countries share their research data feed intake of dairy cows and on behalf of the Dutch AI organizations he coordinates the national genetic evaluation for the Netherlanders and Flanders.

**Garry Waghorn:** Senior Scientist at DairyNZ, Hamilton, New Zealand. Garry’s interests centre around nutrition and digestive physiology in sheep and cattle at both the basic and applied level but with a strong focus on environmental sustainability. His current research includes factors affecting feed quality, feed conversion efficiency in dairy cows (residual feed intake) and measurement of methane emissions for inventory and mitigation. Garry’s research objectives are to maximise the efficiency of forage use for production, minimise environmental impacts of farming, and reduce energy losses to methane. He believes that any type of methane mitigation must be profitable to be adopted by farmers, which may be our greatest challenge.

**Eileen Wall:** Scientist, Sustainable Livestock Systems Group, SAC, Scotland. Eileen’s specialist area is animal breeding, genetics, modelling and biostatistics. Her research interests include climate change and livestock systems (impacts, mitigation and adaptation), genetics of fitness traits, development of sustainable and environmental breeding goals and improvements to national genetic evaluations and understanding trade-offs/interactions in livestock systems.

**Other attendees**
In addition to the speakers identified above, there were also NZ, Australian, international scientists, and industry representatives from NZ and Australia present (see the full list of attendees in Appendix 3).
Prior to the Workshop, a Discussion Document was written and circulated to all participants (see Appendix 2). A list of participants, and their affiliations are attached as Appendix 3.

The Workshop was broken into 3 half-day formal presentation sessions around CH\textsubscript{4} and RFI research in the different countries represented. The 4\textsuperscript{th} session involved short formal presentations followed by an extended discussion session. A summary Workshop Proceedings is attached as Appendix 4.

Handout copies of each presentation are attached as Appendices 5-8.

During the Workshop, participants were asked to identify what they wanted from the workshop, and what their priority was (see Appendix 9).

In addition, a free access whiteboard was made available (see Appendix 10). At the end of the two days, the following strapline was generally accepted as an appropriate summary.

“THE WHOLE IS THE PRODUCT OF THE PARTS”

Prior to the Workshop, some speakers provided references to supplement their presentations (see Appendix 11).

Contact details for all participants are attached as Appendix 12.

Session 1: Measuring CH\textsubscript{4}
Chair: Dr Graeme Attwood (New Zealand)

1.1 Measurement of enteric methane emissions from cattle
Dr Roger Hegarty/ Dr Dorothy Robinson (Australia)
Presentation of recent Australian data in the area of enteric CH\textsubscript{4} measurement in cattle (and sheep).

1.2 Measurement of enteric methane emissions from sheep
Dr Cesar Pinares (NZ)
Recent New Zealand data related to measuring CH\textsubscript{4} emissions in sheep were presented and discussed.

Chairman’s summary Session 1: Collaboration
- We need the ability to bring and share data – how do we achieve this?
- There is a need to organise specific workshops with data

Methodologies
- Are protocols limiting?
- Methane measures for different countries – how do we rationalise protocols?
- Can we find a way to share resources?

Moving forward
- An end point for Animal Genetics use is a simple, accurate test
- Microbial Genomics/Animal Genomics are two components with massive amounts of information need to start thinking how to connect the two.
- We also require the input of Modelling groups.
Session 2: Measuring RFI
Chair Prof Phil Vercoe (Australia)

2.1 Efficiency in cattle
Dr Donagh Berry (Ireland)
The need for clear and definitive research goals and phenotypes was discussed. The presentation also emphasised the overall herd or flock rather than individual animal performance.

2.2 Canadian Efforts into Factors Underlying RFI and Methane Production
Prof Steve Moore (Canada)
An overview of current Canadian RFI research and its association with CH₄ emissions. The impact of GxE interactions was also highlighted as well as work around DNA markers for RFI and research into rumen microbial environment in relation to both CH₄ emissions and RFI.

2.3 Feed Efficiency Research University of Wyoming
Dr Kristi Cammack (USA)
A comprehensive summary of the Growsafe RFI system designed specifically for sheep, along with current data from the University of Wyoming research programme.

2.4 Maternal efficiency, residual feed intake and methane in sheep
Dr Andrew Thompson (Australia)
Sheep CRC ‘Transforming sheep and their management’ programme research investigating how efficiency can be improved by selecting for ewes with resilient genotypes and/or eat less feed, yet perform at the same level.

2.5 Measuring residual feed intake (RFI); the feed conversion efficiency trial
Dr Garry Waghorn (NZ)
A discussion around all aspects of the continuum; methane emissions, measuring feed intake and rumen function.

Chairman's summary Session 2:
Collaboration
● need to get together to quantify scope of RFI
● need for a working group on lactating animals

Methodologies
● there is a lack of information related to sheep RFI
● what is the role of behaviour in that trait?

Moving forward
● need to learn from the RFI experience
● need information in the same format on the relationship between RFI and Methane
● GxE interaction – need a better handle, sharing data would help
● further discussion on working groups required
Session 3: Genotyping and Analysis  
Chair: John McEwan

3.1 Scene setting  
Dr Peter Amer (NZ)  
A scene setting presentation for a session on genotyping and analysis, which covered what actually drives selection and how data should be presented when publishing.

3.2 Validating and standardising rumen microbial community analysis  
Dr Sandra Kittelmann (NZ)  
This presentation discussed the rumen and analysis of rumen microflora along with current research related to identifying the variety of microorganisms present in the rumen that are involved in CH₄ emissions.

3.3 DNA sampling of the animal  
John McEwan (NZ)  
A brief introduction to the different methods for collecting and storing DNA.

3.4 Genetics of GHG associated traits in sheep & beef cattle  
Dr Dominique Francois (France)  
A presentation of current results from French CH₄ and RFI research in both sheep and cattle.

3.5 Traits Correlated with Sheep Methane Emissions  
Dr Dorothy Robinson (Australia)  
An overview of Australian work on traits correlated with CH₄ emissions in sheep from a number of different research programmes.

3.6 Breeding goals to reduce GHG emissions  
Dr Eileen Wall (United Kingdom)  
A discussion on how breeding goals can contribute to reducing ruminant greenhouse emissions with reference to current work in the UK.

Chairman’s summary Session 3:  
Collaboration  
● Every country’s Industry structure is different  
● a challenge is to determine how signals get back to breeders to motivate making changes  
● can we learn from each other?

Methodologies  
● This session gave a good indication of the traits, measurements and how to use them  
● There is a need to re-jig existing selection criteria for reduction in emissions intensity  
● How to define traits between CH₄ and RFI

Moving forward  
● Sampling - more needed in traditional molecular side  
● meta data and raw sequencing data could be revisited and reanalysed  
● Propose go ahead and collect DNA samples as a standard  
● Are rumen samples taken, need to await agreed collection protocol?
Session 4: Moving Forward
Chair: Mark Aspin
Three brief presentations were followed by a combined discussion at the end of the session.

4.1 Trait Prioritisation
   John McEwan (NZ)
   An overview of the different traits and co-traits that are involved in CH4 and RFI research.

4.2 Ruminant Production of CH4: What’s EMBRAPA up to?
   Dr Alexandre Caetano (Brazil)
   An overview of the extent of EMBRAPA as a domestic and International entity plus a summary of recent research data.

4.3 Data Sharing
   Roel Veerkamp (Netherlands)
   A summary of recent research data from The Netherlands, and the principles of data sharing involving large data sets and multiple research collaborations using the RobustMilk project as an example.

Chairman's summary Session 4: Collaboration
- The common opinion was “Yes” to a network.
- The question posed was “How do we keep going?”

Methodologies
- Establish and recognise points of focus for Dairy/Beef/Sheep
- Desire for a network of experiences/protocols etc

Moving forward
- Format of the Network
  - does it need formalised
  - who’s responsible
  - how to communicate
  - how to bring in new people
  - what are the aims and specific actions on an immediate short term basis
- Areas that require more networking - Genetics/Nutrition/Microbes/Breeding Goals
SECTION 4  KEY ISSUES

During the discussions in Session 4, a number of Key Issues were identified. These are applicable to all GRA member parties, and were seen as the areas requiring attention in the short term.

These issues therefore form the basis of the Action points that are to be addressed as a result of the Workshop.

Methodologies

Protocols
There are benefits from systems where shorter and easier and maybe less accurate measures are taken at longer intervals, but with more repeats to dilute out error.

The problem with long continuous tests is that they record the same semi-permanent errors day after day, and so the noise associated with these fouls up the prediction and so that things that look consistent over a test period do not hold up in a different time, place or situation.

'Butterboxes'
Enable measurements to be taken in the field. The animals are enclosed only for short time periods and the results have good correlation with respiration Chambers. However they have welfare considerations; perhaps a cheap re-breathing system is required? There is still a need for respiration chambers to ‘calibrate’. There is also a need to test the CH₄ relationship to intake, which with butterboxes is an unknown.

Rumen sampling
The NZAGRC research programme is examining all steps of rumen sampling and sequencing and first step results should be available by November 2012. At that time formal sampling protocols can be drawn up and circulated for comment.

Analysis and reporting
It is important that authors compute and report basic statistics and key genetic parameters for all component traits when reporting residual feed intake studies.

There is merit in studying and reporting residual feed intake because it provides a clearer perspective on underlying biology linked to differences in maintenance requirements.

However, animal breeders will commonly prefer to work with component traits when designing, upgrading and/or deploying genetic evaluation systems. For this reason, it is very important to publish genetic parameter details about component traits of residual feed intake, and their genetic and phenotypic relationships with residual feed intake.

Industry support

It was identified that a key issue will be how information is presented to the industry.

There was general agreement that if rapid industry uptake is to occur, then reducing emissions intensity per unit of output was the most economically effective outcome; as opposed to reducing total emissions per individual.

A further point is that the industries are different in each country. Industry structure will have a large effect on uptake of both RFI and CH₄ Research.
Networking
The common ground was that a network is an imperative. A number of areas were identified as important.

In the first instance the setup and maintenance of an email group
- Email group – informal communication a very good way of sharing of ideas and information via email discussion list.
- Website forum for communication
- Semi-regular phone conferences
- Establish a list of topic areas/people
- Don’t try and do everything – identify one or two things to address
- Structure with a good secretary to organise phone ups etc
SECTION 5  ACTION POINTS IDENTIFIED

Projected responsibilities are indicated in red beside each action point. However, these are not definitive, and may be modified or reassigned with time as the network is established.

1. **Next Workshop in Australia**
   Timed to link up with an international meeting that most will attend, possibly April 2012
   Workshop to be based round “Defining traits”
   Julian Hill

2. **The Network – what’s needed**
   - Appoint individuals as sub-group coordinators
     - Microbial
     - CH₄
     - RFI
     - Systems
     - Genetic improvement
     - Adoption
   - Email group discussion list
   - Website forum for communication
   - Semi-regular phone conferences
   - Write up of this workshop (circulated for comment)
   - List of topic areas/people
   - stock-take existing research projects
   - Stock-take of data
   - genetic linkages across experiments

3. **Who else should be involved/linked**
   - other researchers to be approached?

4. **White paper**
   draft due mid August

5. **Key initiatives:**
   - trait definition for intake
   - Protocols endorsed by GRA
   - summary of current experiments
   - Rumen microbial studies
   - Systems level interactions – modelling etc

6. **Other associated groups that are essential to link to**
   - sub-group coordinators
   - Caliberation between methods
   - Activities that are signalled out of the white paper
   - Candidates for methane emissions
   - Correlated traits

7. **Measurement challenge**
   - Sound Protocols
   - Calibration between methods
   - Activities that are signalled out of the white paper
   - Candidates for methane emissions
   - Correlated traits

8. **“Quantify how much it will make a difference”**
   - what are the adoption issues?
   - will uptake get industry support?

9. **Future projects**
   on going; to be addressed in White Paper
Appendices to:

Contract GRA1001
International Workshop:
Enteric CH\textsubscript{4} mitigation using animal selection, genetics and genomics

16-17 May 2011
Auckland, New Zealand

Draft Report June 2011

Grant Shackell
John McEwan
GLOBAL RESEARCH ALLIANCE
International Workshop
16-17 May 2011
Auckland, New Zealand

Organised by:
Grant Shackell
Victoria Bradley
Kate Parlane
John McEwan

AgResearch
NZAGRC
NZAGRC
AgResearch

Funding sources
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All photographs and diagrams were provided courtesy of the speakers and are taken from their presentations.

All responsibility for any remaining errors or omissions rests with the authors.

Disclaimer
This report has been commissioned by the New Zealand Government to support the goals and objectives of the Global Research Alliance on Agricultural Greenhouse Gases. While every effort has been made to ensure the information in this publication is accurate, the Global Research Alliance does not accept any responsibility or liability for error of fact, omission, interpretation or opinion that may be present, nor for the consequences of any decisions based on this information. Any view or opinion expressed does not necessarily represent the view of the Global Research Alliance.
APPENDIX 1 WORKSHOP DISCUSSION DOCUMENT

If this document is being read electronically, the Pre-Workshop Discussion Document can be opened by double clicking anywhere on the image below.

Research to mitigate enteric CH₄ emissions from ruminants using Animal selection, Genetics and Genomics

A discussion document prepared for participants in a Global Research Alliance International Workshop 16th-17th May 2011, Auckland, New Zealand
## Appendix 2 Workshop Participants

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<thead>
<tr>
<th>Name</th>
<th>Affiliation</th>
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<tr>
<td>Peter Amer</td>
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<tr>
<td>Mark Aspin</td>
<td>PGgRC, New Zealand</td>
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<tr>
<td>Graeme Attwood</td>
<td>AgResearch, New Zealand</td>
<td>Chair</td>
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<tr>
<td>Alexandre Caetano</td>
<td>EMBRAPA, Brazil</td>
<td>Speaker</td>
</tr>
<tr>
<td>Kristi Cammack</td>
<td>University of Wyoming, USA</td>
<td>Speaker</td>
</tr>
<tr>
<td>Harry Clark</td>
<td>NZAGR, New Zealand</td>
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</tr>
<tr>
<td>Steve Davis</td>
<td>ViaLactia, New Zealand</td>
<td>Observer</td>
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<tr>
<td>Tom Davison</td>
<td>Meat &amp; Livestock, Australia</td>
<td>Observer</td>
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<tr>
<td>Dominique Francois</td>
<td>INRA, France</td>
<td>Speaker</td>
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<td>John Goopy</td>
<td>Department of Primary Industries, Australia</td>
<td>Observer</td>
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<tr>
<td>Roger Hegarty</td>
<td>Beef Industry Centre, Australia</td>
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<tr>
<td>Dorothea Heimeier</td>
<td>ViaLactia, New Zealand</td>
<td>Observer</td>
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<td>Julian Hill</td>
<td>MLA Australia</td>
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<tr>
<td>Sandra Kittelmann</td>
<td>AgResearch, New Zealand</td>
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<tr>
<td>Klaus Lehnert</td>
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<td>Cameron Ludemann</td>
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<tr>
<td>Lynette Mitchell</td>
<td>AgResearch, New Zealand</td>
<td>Secretary</td>
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<tr>
<td>Stephen Moore</td>
<td>Dept of Ag, Food and Nutritional Science, Canada</td>
<td>Speaker</td>
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<tr>
<td>Hutton Oddy</td>
<td>University of New England, Australia</td>
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<td>Cesar Pinares</td>
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<tr>
<td>Andrew Thompson</td>
<td>Dept of Agriculture and Food, Australia</td>
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<td>Roel Veerkamp</td>
<td>Wageningen University, The Netherlands</td>
<td>Speaker</td>
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<tr>
<td>Philip Vercoe</td>
<td>The UWA Institute of Agriculture, Australia</td>
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<tr>
<td>Garry Waghorn</td>
<td>DairyNZ, New Zealand</td>
<td>Speaker</td>
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<tr>
<td>Eileen Wall</td>
<td>Scottish Agricultural College, Scotland</td>
<td>Speaker</td>
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<tr>
<td>Guangyong Zhao</td>
<td>China Agricultural University (CAU), China</td>
<td>Observer</td>
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APPENDIX 3 WORKSHOP PROCEEDINGS

Introduction
Dr Harry Clark (NZAGRC)
Dr Clark discussed the background to the Global Research Alliance and summarised the charter from the inaugural meeting in April 2010. From that meeting three groups were formed - Livestock Research Group, Croplands Research Group and Rice Research Group. The Livestock Research Group met in Banff and a number of projects were identified as priority for the GRA and included setting up a network around animal breeding approaches to reducing methane emissions.

The GRA does not have a central funding mechanism; therefore, individual participants have to find their own resources. The purpose of this Workshop is to have collective discussions about sharing data and ideas, moving forward and working together to enable outcomes that wouldn’t have been able to be achieved individually.

Session 1: Measuring CH₄

Chair: Graeme Attwood

1.1 Measurement of enteric methane emissions from cattle
Roger Hegarty/Dorothy Robinson (Australia)
Drs Roger Hegarty and Dorothy Robinson combined to present recent data from Australia in the area of enteric CH₄ measurement in cattle and sheep.

The presentation worked through SF6 (see Figure 1a), head hoods (Figure 1b) and respiration chamber (Figure 1c) studies and touched on the feed/DM intake question.

Variability between measurements on the same animals was flagged during the presentation.

As part of the presentation the following questions were raised:
- Phenotype— do we need to measure with high precision over a short time or better to accept lower precision at a single measurement time and measure repeatedly?
- Dry matter intake is related to genetics – do we need to measure it as well?
- what is the merit of measuring methane 3 or 4 times in a row, one day after the other?
- do we really need to have a measure of methane production from a defined measure of feed intake – with the prospect of doing on thousands of animals in coming years?
- what are the merits of the butterbox (a cheap non re-circulating chamber for measuring methane production over short periods)?

During the presentation the concept of the ‘butterbox’ (see Figure 1d) for measuring CH₄ in sheep was also raised. The ‘butterbox’ is a Polycarbonate booth (790 litres) which is a sealed container (with a rubber mat on floor) that has no circulation. Its use is limited to 1 hour, and utilises the sheep’s elevated physiological capacity to bind oxygen compared to cattle. The main cause of loss of measurements occurs with the sheep jumping up and breaking the seal.
1.2 Measurement of enteric methane emissions from sheep

Cesar Pinares (NZ)

Dr Cesar Pinares’ presentation also worked through the development of CH₄ measurement technologies (see Figure 2). Data from New Zealand studies on sheep, all measured using respiration chambers, were presented and discussed.

Again the variation between measurements and feed types was on the same animals was highlighted. However, ranking differences between animals remain relatively consistent within that variation.

Dr Pinares summary stated:

- Emission differences between animals are repeatable across time and diets, and heritable
- No evidence to date that CH₄ yield (gCH₄/kgDMI) is associated with production traits
- Animal variation offers a potential solution to reducing livestock methane emissions

But

- Is CH₄ g/kg DMI a sound trait; is it related to animal efficiency?
- Is the measurement protocol appropriate, what other practical alternatives are there?
- How can we exploit the selection line resources to understand mechanisms?
Figure 2: The development of techniques for CH₄ measurement

1960s \[ \rightarrow \]
   To improve energy efficiency
   \( (\text{CH}_4 \text{ loss of } 2-12\% \text{ of } \text{GEI}) \)
   -Indirect calorimetry, use of chambers-

1970s \[ \rightarrow \]

1990s \[ \rightarrow \]
   Focus on GHG emissions
   -use of SF₆ tracer technique-
   but

today \[ \rightarrow \]
   -respiration chambers-

Session 1 Chairman’s summary:

**Collaboration**
- We need the ability to bring and share data – how do we achieve this?
- There is a need to organise specific workshops with data

**Methodologies**
- Are protocols limiting?
- Methane measures for different countries – how do we rationalise protocols?
- Can we find a way to share resources?

**Moving forward**
- An end point for Animal Genetics use is a simple, accurate test
- Microbial Genomics/Animal Genomics are two components with massive amounts of information need to start thinking how to connect the two.
- We also require the input of Modelling groups.
Session 2 Measuring RFI
Chair Prof Phil Vercoe (Australia)

2.1 Efficiency in cattle
   Donagh Berry (Ireland)
Dr Donagh Berry spoke about his work from Ireland, via Skype, with his slides being controlled from the meeting room.

The presentation highlighted that research goals and phenotypes are not necessarily clear and definitive. Outside the immediate research environment, the rationale for conducting feeding efficiency research, whatever the end goal, is often placed around the overall herd or flock rather than on individual animal performance.

The presentation had a clear practical on-farm component, and highlighted the type of information the industry is interested in (see Figure 3).

Dr Berry identified Ireland’s position in having good linkages with New Zealand, Netherlands and Canada for dairy (and therefore other countries given co-linkage) and France, the UKK and Canada for beef. The Irish resource has good access to large numbers of well phenotyped animals, and utilises a largely pastoral grazing system. In addition, there is a good DNA resource in the Irish industry.

In his summary Donagh identified:
- the need for a clear definition of phenotype before we do the fancy stuff … especially for cows
- a need to take cognisance of end use including the system components
- that there are implications also for CH₄ derived traits – a residual type trait is commonly used but is it best?

Figure 3: Typical results from an RFI experiment and industry application

![Figure 3: Typical results from an RFI experiment and industry application](image-url)
2.2 Canadian Efforts into Factors Underlying RFI and Methane Production
Steve Moore (Canada)

Prof Steve Moore provided an excellent overview of the current state of play in Canada with regards to both RFI research and its association with CH\textsubscript{4} emissions.

Amongst the information presented was a description of how biological mechanisms contribute to between animal variation in RFI (see Figure 4).

The contribution of the impact of GxE interactions on the measurement of RFI was also highlighted. Recent data show that re-ranking of animals with respect to RFI can be due to season, maturity and diet.

Work around DNA markers for RFI was discussed, along with research related to rumen microbial environment and both CH\textsubscript{4} emissions & RFI.

Steve’s summary identified:

- a clear need to develop SOPs to ensure consistency of phenotype for both RFI and CH\textsubscript{4} production
- Industry structure will have a large effect on uptake of both RFI and CH\textsubscript{4} Research
- cattle feed efficiency was associated with the presence or absence of particular bacteria in the rumen
- rumen bacterial PCR-DGGE patterns tend to be grouped based on L-RFI only under high energy diets
- no such grouping trend was observed for methanogens

Figure 4: Biological mechanisms contributing to variation in RFI (after Richardson and Herd, 2004; Herd et al., 2004)
2.3 Feed Efficiency Research University of Wyoming
Kristi Cammack (USA)

Dr Kristi Cammack presented a comprehensive summary of the Growsafe RFI system. The Wyoming system is the first designed specifically for sheep, albeit adapted from a cattle system.

One consideration of RFI research was the re-ranking of animals on different diets. Dry matter digestibility was similar among RFI groups (high RFI; medium RFI; low RFI), differences in feed efficiency were 10% greater on maintenance than grower diet, but RFI rankings on ewe grower and maintenance tests were not the same (see Figure 5).

The University of Wyoming also has collaboration with Montana State to evaluate rumen microbial ecology in the sheep.

Kristi’s summary points were:
- Low and high efficiency ewes had similar gains (0.75 lb/day).
- Low efficiency ewes consumed ~20% more feed.
- Ewes that were more feed efficient spent 25% less time at the feed bunk
- RFI appears to not be related to growth and wool traits
- High efficiency ewes had lower number of lambs born EPDs than low efficiency ewes
- Twin born ewes had less desirable RFI values
2.4 Maternal efficiency, residual feed intake and methane in sheep

Andrew Thompson (Australia)

Dr Andrew Thompson discussed aspects of the sheep CRC ‘Transforming sheep and their management’ programme that fit with efforts to reduce GHG emissions from sheep.

The programme seeks to enhance reproductive output, improve maternal efficiency by increasing Kg lamb weaned per kg ewe joined and mating yearling ewes to increase lifetime production.

Andrew presented research investigating how efficiency can be improved by selecting for ewes that do better over summer (resilient genotypes), also has links to adaptation. A further area for improvement is breeding for ewes that eat less feed, yet perform at the same level (efficiency of feed use; see Figure 6).

In summary, Andrew noted that:

- there is scope to improve maternal efficiency through better management and genetics
- improving maternal efficiency will reduce CH_4 emissions intensity
- links between residual feed intake & methane emissions are unclear
  - further analysis needed
- a simple, easy use CH_4 measurement technique is an imperative

Figure 6: Indoor feed measurement facility
2.5 Measuring residual feed intake (RFI)
    Garry Waghorn (NZ)
Dr Garry Waghorn’s presentation at the end of Day 1 was an opportunity to discuss the Workshop topic from all aspects of the continuum; methane emissions, measuring feed intake and rumen function.

A basic concept is that animals are not equal (see figure 7).

From his extensive experience, Garry was able to identify areas where the practicalities of research in these areas may result in a need for some soul searching. He was also able to stress those areas where careful and meticulous planning and execution are required, and how some pitfalls can be avoided.

Figure 7: Individual difference in feed intake for the same weight gain
Session 2 Chairman’s summary:

**Collaboration**
- need to get together to quantify scope of RFI
- need for a working group on lactating animals

**Methodologies**
- there is a lack of information related to sheep RFI
- what is the role of behaviour in that trait?

**Moving forward**
- need to learn from the RFI experience
- need information in the same format on the relationship between RFI and Methane
- GxE interaction – need a better handle, sharing data would help
- further discussion on working groups required
Session 3: Genotyping and Analysis
Chair: John McEwan

3.1 Scene setting
Peter Amer (NZ)
Dr Peter Amer’s task was to set the scene for a session on genotyping and analysis.

The focus of the Workshop was Enteric CH₄ mitigation using animal selection, genetics and genomics. For this to be effective, it is first essential to understand what actually drives selection (see Figure 8).

The take home messages were:
- all raw measurements should be recorded and appropriate summaries should be displayed in any published articles
  - report raw results in addition to your favourite transformations
  - show h² for methane time versus methane yield
  - estimate and report raw feed intake results, and all of the adjustments to get residual feed intake
  - estimate and report parameters for raw feed intake at the same time as for residual feed intake
- low cost phenotypes for both Methane Yield and residual feed intake are an imperative
- Methane traits will get more traction within the decision making of commercial breeding programs when
  - they are complementary to farm profitability
  - there is some sort of society or consumer “pull through” incentivising farmers to purchase low methane emission genetics

Peter concluded that there are opportunities to fine tune current genetic improvement pipelines to reduce GHG emissions intensity. He also identified a need for genetic improvement pipelines to maximise the advantages from new measurement technologies and discoveries in the methane and residual feed intake area.

Figure 8: What drives selection?
- Visual characteristics of animals
- Farm profit
- Animal welfare
- GHG emissions
- Environmental impacts
3.2 Validating and standardising rumen microbial community analysis
Sandra Kittelmann (NZ)

Dr Sandra Kittelmann discussed the rumen and analysis of rumen microflora.

The rumen ecosystem harbours a variety of microorganisms such as Bacteria, fungi and ciliate protozoa, which ferment the ingested feed and deliver readily accessible nutrients to the host animal (Fig. 9).

Methanogenic archaea use the large amounts of hydrogen produced by fermentation to gain energy from the reduction of carbon dioxide to methane. The community structure of these different groups of microorganisms has been found to be influenced by the host's diet and is itself thought to contribute to shaping the host CH₄ emission and feed conversion phenotype. The rumen microflora is therefore of interest to both CH₄ and RFI studies. Despite this, rumen contents are not collected routinely in either. Current research is aimed at understanding the structure and function of rumen microbial communities by using high-throughput sequencing of phylogenetic marker genes. While validation and standardisation of this approach is still in the development phase, there is merit in routinely co-collecting rumen samples within CH₄ and RFI protocols for later analysis.

Sandra outlined the workflow for analysing microbial community structure in rumen samples (see diagram right).

There are several different rumen sample collection methods (rumenocentesis, stomach tubing, fistulation), which offer different sample volumes and have different levels of invasiveness.

The challenge is to identify and evaluate the biases and to be aware of them when interpreting results. It is important to follow standardised protocols when collaborating internationally.

Once the sample has been processed, and DNA extracted, analysis is carried out based on phylogenetic marker genes, such as 16S rRNA genes, which offer high phylogenetic resolution and a broad range of available reference sequences to establish robust taxonomic framework for species assignment.

The sequencing data is then passed through a series of QC parameters and analysis steps, which should be validated and standardised to allow between lab comparisons.

Sandra’s summary was that they are undertaking a research programme into examining all steps of rumen sampling and sequencing and that first step results should be available by November 2012 and at that time formal sampling protocols can be drawn up and circulated for comment.
3.3 DNA sampling of the animal
John McEwan (NZ)

John McEwan briefly introduced the different methods for collecting and storing DNA.

His take home message was that there are different requirements for DNA quantities and qualities for the various genomic technologies that are currently available (see Figure 10).

In addition, he stressed the need for accurate recording protocols and the need for careful consideration of DNA preparation methodologies in order to ensure that the quality is preserved.

- the new technologies do not like degraded DNA!!!!
- don’t fiddle around with picogreen... Run a gel
- storing frozen tissue is asking for a power failure!
- make sure the animal ID matches the phenotype record!

Figure 10: DNA quantity and quality required for different genomic analysis methods

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<th>Method</th>
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3.4 Genetics of GHG associated traits in sheep & beef cattle  
Dominique Francois (France)  
Dr Dominique Francois presented current results from French CH$_4$ and RFI in both sheep and cattle (see figure 11).

Results from a sheep RFI study on animals selected for divergent for low or high RFI showed differences in terms of live-weight and growth (0.2sd) and the differences were in line with predictions based on genetics estimates.
- the low RFI group ate significantly less hay and pellets than the high group

Cattle CH$_4$ production, measured using SF6 tracer technology showed
- repeatability =0.77 intra period but 0.17 inter period
- a weak relationship between CH$_4$ production (as L/d or L/kg LW gain) and residual feed intake = 0.06
- a $+0.20$ correlation between CH$_4$ production and DM intake
- that the relationship between RFI and CH$_4$ production may be low when animals are not selected for feed efficiency

Figure 11: French feed intake facilities

3.5 Traits Correlated with Sheep Methane Emissions  
Dorothy Robinson (Australia)  
Dr Dorothy Robinson presented an overview of Australian work on traits correlated with CH$_4$ emissions in sheep on behalf of a number of colleagues.

This research adopts a Multi-pronged approach:
- identify animals producing less CH$_4$/unit of intake, & investigate why (e.g. rumen fauna)
- identify animals that produce less CH$_4$ per unit of growth or production, either because they produce less CH$_4$ per unit of feed intake, or other reasons (greater efficiency, diet selection in the paddock)
- identify which conditions are most likely influence the expression of between animal differences (repeatabilities/heritabilities)
- Use this information to develop the most suitable test protocols
- Combine with multi-trait selection indices to maximise benefit
The programme is also directed towards developing a simple technology to enable ovine CH$_4$ emissions in the field.

Dorothy also presented data in relation to use of the ‘Butterbox’ (see Figure 12), compared to respiration chambers. The ‘Butterbox’ concept captured a metaphorical “novel approach award” for capturing the most interest during the Workshop.

**Figure 12:** ‘Butterbox’ for measurement of CH$_4$ emissions in sheep

- the ‘Butterbox’ provides a reasonably accurate ‘snapshot’ of CH$_4$ emissions
- Respiration Chambers are more expensive to construct and run but;
  - allow longer measurement periods
  - standardised feed protocols reduce variability
- results depend on the behaviour of the animal, e.g. diet, amount eaten, rumen microbes, in both systems
- in Western Australia, ‘Butterbox’ measurements taken soon after a Respiration Chamber measurement are a better predictor of Chamber measurements than a repeat Chamber measurement 4 weeks later
- grazing sheep select when and what to eat – some datasets show an intriguing sire & sire type differences that are worth investigating further

### 3.6 Breeding goals to reduce GHG emissions
**Eileen Wall (United Kingdom)**

The final presentation in the session’ from Dr Eileen Wall, built on Peter Amer’s introduction by discussing how breeding goals can contribute to reducing ruminant greenhouse emissions.

By presenting a diagram of greenhouse gas emissions from livestock systems (see figure 13), Eileen covered different ways of establishing breeding goals.

1. **Breeding for improved efficiency of the animal**
   - Production & gross efficiency = fewer animals for a given production level
   - there has been an 8% drop in UK emissions due to declining dairy numbers, better animal efficiency is required to offset this

2. **Breeding for improved efficiency of the system**
   - “Functional” traits can reduce wastage from the system & therefore GHG emissions
   - Improved dairy fertility could potentially reduce methane emissions by 10-15%

3. **Breeding for reduced GHG emissions**
   - Identify “high” or “low” GHG emitters (on different diets and systems!)
   - many “economic” breeding goals have a correlated effect of reducing emissions intensity
   - a 0.4 to 1.4% reduction in kg CO$_2$e/breeding animal/year annum is possible in many ruminant species

Livestock genetic improvement has a role in reducing greenhouse gas emissions. Breeding goals (and associated tools) can help to reduce emissions intensity (per country, per animal, per unit product), but there are several riders that require consideration.
The use of "Environmental" breeding goals that could reduce GHG emissions from ruminant livestock will come at an economic cost to the farmer. Furthermore, some production selection goals have impacts on health, fertility and welfare and Industry structure may preclude an equitable distribution across all producers.

The limiting factor therefore is how to maximise farmer/producer uptake of any genetic and genomic tools for the mitigation or intensity reduction of enteric CH$_4$ emissions from ruminant livestock.

**Figure 13: Greenhouse Emissions from Livestock Systems**

**Session 3 Chairman’s summary:**

*Collaboration*
- Every country’s Industry structure is different
- A challenge is to determine how signals get back to breeders to motivate them to make changes
- Can we learn from each other

*Methodologies*
- This session gave a good indication of the traits, measurements and how to use them
- There is a need to re-jig existing selection criteria for reduction in emissions intensity
- How to define traits between RFI and CH$_4$

*Moving forward*
- Sampling - more needed in traditional molecular side, meta data and raw sequencing data could be revisited and reanalysed
- Propose go ahead and collect DNA samples as a standard
- Are rumen samples taken, need to await agreed collection protocol?
Session 4: Moving Forward
Chair: Mark Aspin

4.1 Trait Prioritisation
John McEwan (NZ)
John McEwan presented a brief overview of the different traits and co-traits that are involved in CH4 and RFI research, as a pre-cursor to an extended combined discussion at the end of the session.

The list included:
Usually $ driven and require information on:
- Economic index
- Objective traits
- Predictor traits
  - genetic correlations
  - phenotypic correlations
  - heritability
  - variation
- require a shadow price for carbon (aka methane emission cost)

CH4
An objective trait, for which ~kg DMI/breeding animal/yr is currently used as a proxy
- Respiration Chamber (accurate but expensive) not clear if fixed or ad-lib feeding should be used
- Portable Chambers (cheap, repeatable, moderate correlation) can be used with grazing animals but most suitable for sheep and no associated intake can be easily measured on pasture
- Laser or C-Lock suitable for dairy cattle on daily milking and for use in residual feed intake facilities.

Intake
An objective trait, for which liveweight is often used as a proxy
- Spot measurement as per CH4 production measurement
- Period... RFI
- Both approximations of kg DMI/breeding animal/year

Systems Used affecting emissions intensity
- Production traits
  - growth/carass
  - reproduction (puberty)
  - disease
  - longevity
  - milk
- Effect of diet and farm system
  - ME (C4/C3 grasses)
  - Pasture Composition
  - feeding level (ad lib, restricted)
  - age (GxE)
4.2 Ruminant Production of CH₄: What’s EMBRAPA up to?
Alexandre Caetano (Brazil)
Dr Alexandre Caetano’s presentation introduced the extent of EMBRAPA; both as a domestic and International entity as well as recent research data.

In addition, he identified as part of the Moving Forward process the need to establish common protocols along with a need for better modeling of the trait (see Figure 14)

There is also a need to establish differences in the rate of CH₄ production during production phases (Young x Feeder x Mature x Lifetime) and how these are correlated.

Figure 14: Example model for CH₄ emission research

4.3 Data Sharing
Roel Veerkamp (Netherlands)
Dr Roel Veerkamp presented recent research data from the Netherlands. He demonstrated the large impact that genetics can make on reducing methane emissions, using predicted methane from DMI. With genomic selection and sharing data in a reference population, a 30% reduction in 20 years seems achievable.

The presentation also covered Roel’s extensive experience in data sharing involving large data sets and multiple research collaborations. The RobustMilk project was used as an example (see Figure 15).

In general summary Roel indicated that intake was a strong predictor of methane emission and that reducing methane emissions intensity closely followed increasing production per unit of intake.
APPENDIX 4 POWERPOINTS SESSION 1
If this document is being read electronically, the Pre-Workshop Discussion Document can be opened by double clicking anywhere on the image below.
APPENDIX 5  POWERPOINTS SESSION 2

If this document is being read electronically, the Pre-Workshop Discussion Document can be opened by double clicking anywhere on the image below.
APPENDIX 6  POWERPOINTS SESSION 3

If this document is being read electronically, the Pre-Workshop Discussion Document can be opened by double clicking anywhere on the image below.
APPENDIX 7  POWERPOINTS SESSION 4

If this document is being read electronically, the Pre-Workshop Discussion Document can be opened by double clicking anywhere on the image below.

6/23/2011
APPENDIX 8 PARTICIPANT COMMENTS

What I want of the GRA:

Collaboration

- Specific data workshops, where people can exchange data and expertise/knowledge to analyse them and develop standardised protocols and/or definitions of traits
- Use the power of shared data to see how close we are to linking animal to microbe – genome and link to CH4 (+ ...)
- Real value is having quant geneticists, microbial ecologists and nutritionists in the same room tracking a complex problem (also cattle, sheep, other scientists)
- Share/pool estimates of genetic variation
- Data sharing – make it easy.
- Build relationships to compose & check results and highlight where information is lacking
- A place to share data and ideas about reducing methane from livestock
- Working together to increase power of data we’re sitting on (or hope to have in future)

Methodologies

- Breeding focus: combine data sets to get statistical power & better parameter estimates
- Data – equivalent across populations (breeds) and countries
- Networking – building a critical mass of people and data
- Resources – need to enable research and collaboration
- Better access to ‘experts’ to improve experiment design, protocols and analysis → success
- Find a decent way of measuring phenotype for CH4
- Decide on protocols/methods & definitions to get comparable data & reduce ambiguity
- Work together to understand complexities of the trait(s) to help quantify potential of different (genetic) tools to reach goal
- Association of low methane animal phenotype (genotype with differences in rumen microbial genes/populations)
- Within each CH4 measuring technique, standards should be set so that everybody can use methods that is best suited but using standardized parameters
- To agree on protocols – common feed (e.g. grass cubes) supplied from Canada, Australia

Moving forward

- Enhanced ability to tackle this difficult issue
- Testing animals under different conditions to consider GxE
- Follow up review in reducing emissions. The problem is that at a high level we have asked what is the low methane trait and how much will this reduce emissions?
- The capability to answer questions, conduct large scale experiments etc that I can’t do as an individual. I have limited resources that can’t accomplish much alone, but can be a part of a bigger picture
- Money/Co-ordination
- A point of leverage for new funding – contribute to global effort – reduced local costs of R&D by sharing relevant data with others
- It’s not yet clear what common ground is
- To be confident that there is valuable application of the CH4 tests/measures we are doing
- To know if/how ‘butterbox’ and respiration chamber data can serve to a common purpose of genetic improvement
- Ensure my research ideas are relevant to others so we want to work together
- To get clear common actions i.e. timeline of activities
- A more clear vision of path to market for genetic solutions for GHG mitigation
- Exchange of experiences – honest discussion of data across borders and helpful advice in both/all directions
**My Priority Action:**

*Collaboration*

- Define the phenotype
- Happy to work with GRA to achieve its goals
- Work with DPI and MLA to determine how best we can share data
- Ensure there’s enough information collect on the animals rumen samples, DNA

**Methodologies**

- Host/microbe interaction
- Follow up with >5 contacts re protocols, analysis, data sharing and unpublished data
- Protocols! I think we need to develop protocols that can be used across different circumstances that still allow data to be effectively combined
- Have a report of paper written which clearly defines the definitions of traits and stipulates how traits should be measured
- Report or write a paper which highlights areas where research is lacking and should be prioritised
- Tools for methane on 2000 cattle
- Tools for Feed Intake on 2000 cattle
- Tidy up butterbox assessment – it’s correlation with chambers; how do the boxes work in the paddock?
- Get protocols for the different measurements for traits
- Don’t focus on defining one and only method but on how to harmonize across methods/experiments
- For the range of approaches to recording which traits (and trait combinations) will make a theoretical difference to make a real industry relevant difference

**Moving forward**

- Try to establish what rumen samples we already have that could be explored in greater detail and pursue what is needed to link genomes. (Need to establish what we have in Aus/NZ (+….) microbe and breeding programs – how can we link these two programs at a level higher than national
- Keep in contact through email, phone, further workshops and potential collaborations.
- Consensus white paper
- International collaboration – clear indication of how NZAGRC/PGGRC can support international collaboration
- Establishing a network so that people get to know each other’s expertise area and can find the appropriate partners for discussion
APPENDIX 9  WORKSHOP WHITEBOARD
APPENDIX 10 FURTHER READING

The following references were supplied prior to the workshop by participants. These were included as pdf files on the workshop flashdrive supplied to all participants.


LUDEMANN C., BYRNE T., SISE J. AND AMER P. Potential for New Zealand farmers to reduce sheep greenhouse gas emissions through genetic selection tools. AbacusBio Ltd


